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#2

RAW SEQUENCE LISTING   DATE: 12/04/2001
PATENT APPLICATION: US/09/850,991   TIME: 13:25:26

Input Set : N:\Crf3\RULE60\09850991.txt
Output Set: N:\CRF3\12042001\I850991.raw

SEQUENCE LISTING
4 (1) GENERAL INFORMATION:
6   (i) APPLICANT: Kossmann, Jens
7   Willmitzer, Lothar
8   Emmermann, Michael
C--> 10   (ii) TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING
11   ENZYMES FROM MAIZE
13   (iii) NUMBER OF SEQUENCES: 4
15   (iv) CORRESPONDENCE ADDRESS:
16   (A) ADDRESSEE: FISH & NEAVE
17   (B) STREET: 1251 Avenue of the Americas
18   (C) CITY: New York
19   (D) STATE: New York
20   (E) COUNTRY: U.S.A.
21   (F) ZIP: 10020-1104
23   (v) COMPUTER READABLE FORM:
24   (A) MEDIUM TYPE: Floppy disk
25   (B) COMPUTER: IBM PC compatible
26   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27   (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)
29   (vi) CURRENT APPLICATION DATA:
C--> 30   (A) APPLICATION NUMBER: US/09/850,991
C--> 31   (B) FILING DATE: 08-May-2001
32   (C) CLASSIFICATION:
38   (vii) PRIOR APPLICATION DATA:
35   (A) APPLICATION NUMBER: 09/148,680
36   (B) FILING DATE: 1998-09-04
39   (A) APPLICATION NUMBER: DE 196 08 918.2
40   (B) FILING DATE: 07-MAR-96
42   (viii) ATTORNEY/AGENT INFORMATION:
43   (A) NAME: Haley Jr., James F.
44   (B) REGISTRATION NUMBER: 27,794
45   (C) REFERENCE/DOCKET NUMBER: GFB-7
47   (ix) TELECOMMUNICATION INFORMATION:
48   (A) TELEPHONE: (212) 596-9000
49   (B) TELEFAX: (212) 596-9090
51 (2) INFORMATION FOR SEQ ID NO: 1:
53   (i) SEQUENCE CHARACTERISTICS:
54   (A) LENGTH: 1993 base pairs
55   (B) TYPE: nucleotide
56   (C) STRANDEDNESS: double
57   (D) TOPOLOGY: linear
59   (ii) MOLECULE TYPE: cDNA to mRNA
61   (iii) HYPOTHETICAL: NO
C--> 63   (iv) ANTI-SENSE: NO
65   (vi) ORIGINAL SOURCE:
66   (A) ORGANISM: Zea mays

ENTERED

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67          (F) TISSUE TYPE: Blattgewebe
69     (ix) FEATURE:
70          (A) NAME/KEY: CDS
71          (B) LOCATION:1..1675
74     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
76 GGC ACG AGG TCA AAA CTC CCT CCA GGG TCA GAT TTG CAA CAA GCT GCA      48
77 Gly Thr Arg Ser Lys Leu Pro Pro Gly Ser Asp Leu Gln Gln Ala Ala
W--> 78    1               5                  10                 15
80 ATT GTG GCT ATT CAG GAA GAG GAC CCT TAT AAT TGG GGG TAT AAC CCT      96
81 Ile Val Ala Ile Gln Glu Glu Asp Pro Tyr Asn Trp Gly Tyr Asn Pro
82              20                  25                 30
84 GTG GTT TGG GGC GTT CCA AAA GGA AGC TAT GCA AGT AAC CCA GAT GGT     144
85 Val Val Trp Gly Val Pro Lys Gly Ser Tyr Ala Ser Asn Pro Asp Gly
86          35                  40                 45
88 CCA AGT CGT ATC ATT GAG TAC CGG CTG ATG GTG CAG GCC TTG AAT CGC     192
89 Pro Ser Arg Ile Ile Glu Tyr Arg Leu Met Val Gln Ala Leu Asn Arg
90       50                  55                 60
92 TTA GGT CTT CGA GTT GTC ATG GAT GTT GTA TAC AAT CAT CTA TAC TCA     240
93 Leu Gly Leu Arg Val Val Met Asp Val Val Tyr Asn His Leu Tyr Ser
94    65                  70                  75                 80
96 AGT GGC CCT TTT GCC ATC ACT TCC GTG CTT GAC AAG ATT GTA CCT GGA     288
97 Ser Gly Pro Phe Ala Ile Thr Ser Val Leu Asp Lys Ile Val Pro Gly
98                  85                  90                 95
100 TAC TAC CTC AGA AGG GAC TCT AAT GGT CAG ACT GAG AAC AGC GCG GCT    336
101 Tyr Tyr Leu Arg Arg Asp Ser Asn Gly Gln Thr Glu Asn Ser Ala Ala
102              100                 105                110
104 GTG AAC AAT ACA GCA AGT GAG CAT TTC ATG GTT GAT AGA TTA ATC GTG    384
105 Val Asn Asn Thr Ala Ser Glu His Phe Met Val Asp Arg Leu Ile Val
106          115                 120                 125
108 GAT GAC CTT CTG AAT TGG GCA GTA AAT TAC AAA GTT GAC GGG TTC AGA    432
109 Asp Asp Leu Leu Asn Trp Ala Val Asn Tyr Lys Val Asp Gly Phe Arg
110     130                 135                 140
112 TTT GAT CTA ATG GGA CAT ATC ATG AAA AAG ACA ATG ATT AGA GCA AAA    480
113 Phe Asp Leu Met Gly His Ile Met Lys Lys Thr Met Ile Arg Ala Lys
114 145                 150                 155                160
116 TCG GCT CTT CAA AGC CTT ACA ATT GAT GAA CAT GGA GTA GAT GGT TCA    528
117 Ser Ala Leu Gln Ser Leu Thr Ile Asp Glu His Gly Val Asp Gly Ser
118              165                 170                175
120 AAG ATA TAC TTG TAT GGT GAA GGA TGG AAC TTC GGT GAA GTT GCG GAA    576
121 Lys Ile Tyr Leu Tyr Gly Glu Gly Trp Asn Phe Gly Glu Val Ala Glu
122              180                 185                190
124 AAT CAA CGT GGG ATA AAT GGA TCC CAG CTA AAT ATG AGT GGC ACT GGG    624
125 Asn Gln Arg Gly Ile Asn Gly Ser Gln Leu Asn Met Ser Gly Thr Gly
126          195                 200                205
128 ATT GGT AGT TTC AAC GAT AGA ATC CGT GAT GCT ATA AAT GGT GGC AGT    672
129 Ile Gly Ser Phe Asn Asp Arg Ile Arg Asp Ala Ile Asn Gly Gly Ser
130     210                 215                 220
132 CCG TTT GGG AAT CCA CTG CAA CAA GGT TTC TCT ACT GGA TTG TTC TTA    720
133 Pro Phe Gly Asn Pro Leu Gln Gln Gly Phe Ser Thr Gly Leu Phe Leu
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Input Set : N:\Crf3\RULE60\09850991.txt
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```
134 225                   230                 235                 240
136 GAG CCA AAT GGA TTT TAT CAG GGC AAT GAA ACA GAG ACA AGG CTC ACG    768
137 Glu Pro Asn Gly Phe Tyr Gln Gly Asn Glu Thr Glu Thr Arg Leu Thr
138              245                 250                 255
140 CTT GCT ACA TAC GCT GAC CAT ATA CAG ATT GGA TTA GCT GGC AAT TTG    816
141 Leu Ala Thr Tyr Ala Asp His Ile Gln Ile Gly Leu Ala Gly Asn Leu
142              260                 265                 270
144 AAG GAC TAT GTA GTT ATA TCT CAT ACT GGA GAA GCT AGA AAA GGA TCT    864
145 Lys Asp Tyr Val Val Ile Ser His Thr Gly Glu Ala Arg Lys Gly Ser
146          275                 280                 285
148 GAA ATT CGC ACC TTC GAT GGC TCA CCA GTT GGC TAT GCT TCA TCC CCT    912
149 Glu Ile Arg Thr Phe Asp Gly Ser Pro Val Gly Tyr Ala Ser Ser Pro
150      290                 295                 300
152 ATA GAA ACA ATA AAC TAC GCC TCT GCT CAT GAC AAT GAA ACA CTA TTT    960
153 Ile Glu Thr Ile Asn Tyr Ala Ser Ala His Asp Asn Glu Thr Leu Phe
154 305                 310                 315                 320
156 GAT ATT ATT AGT CTA AAG ACT CCG ATG GAC CTC TCA ATT GAC GAG CGA   1008
157 Asp Ile Ile Ser Leu Lys Thr Pro Met Asp Leu Ser Ile Asp Glu Arg
158              325                 330                 335
160 TGC AGG ATA AAT CAT TTG TCC ACA AGC ATG ATT GCA TTA TCC CAG GGA   1056
161 Cys Arg Ile Asn His Leu Ser Thr Ser Met Ile Ala Leu Ser Gln Gly
162              340                 345                 350
164 ATA CCA TTT TTT CAT GCT GGT GAT GAG ATA CTA CGA TCT AAG TCG CTT   1104
165 Ile Pro Phe Phe His Ala Gly Asp Glu Ile Leu Arg Ser Lys Ser Leu
166          355                 360                 365
168 GAT CGA GAT TCA TAT GAC TCT GGT GAT TGG TTT AAC AAG ATT GAT TTT   1152
169 Asp Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Lys Ile Asp Phe
170      370                 375                 380
172 ACC TAT GAA ACA AAC AAT TGG GGT GTT GGG CTT CCA CCA AGA GAA AAG   1200
173 Thr Tyr Glu Thr Asn Asn Trp Gly Val Gly Leu Pro Pro Arg Glu Lys
174 385                 390                 395                 400
176 AAC GAA GGG AGC TGG CCT TTG ATG AAG CCA AGA TTG GAG AAC CCG TCG   1248
177 Asn Glu Gly Ser Trp Pro Leu Met Lys Pro Arg Leu Glu Asn Pro Ser
178              405                 410                 415
180 TTC AAA CCT GCA AAA CAT GAC ATT ATT GCT GCC TTA GAC AAA TTT ATT   1296
181 Phe Lys Pro Ala Lys His Asp Ile Ile Ala Ala Leu Asp Lys Phe Ile
182          420                 425                 430
184 GAT ATC CTC AAG ATC AGA TAC TCA TCA CCT CTC TTT CGC CTA ACT ACA   1344
185 Asp Ile Leu Lys Ile Arg Tyr Ser Ser Pro Leu Phe Arg Leu Thr Thr
186          435                 440                 445
188 GCA AGT GAT ATT GTG CAA AGG GTT CAC TTT CAC AAC ACA GGG CCC TCC   1392
189 Ala Ser Asp Ile Val Gln Arg Val His Phe His Asn Thr Gly Pro Ser
190      450                 455                 460
192 TTG GTT CCA GGA GTT ATT GTC ATG AGC ATC GAA GAT GCA CGA AAT GAT   1440
193 Leu Val Pro Gly Val Ile Val Met Ser Ile Glu Asp Ala Arg Asn Asp
194 465                 470                 475                 480
196 AGG CAT GAT ATG GCC CAG ATA GAT GAA ACA TTC TCT TGT GTC GTT ACA   1488
197 Arg His Asp Met Ala Gln Ile Asp Glu Thr Phe Ser Cys Val Val Thr
198              485                 490                 495
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Input Set : N:\Crf3\RULE60\09850991.txt
Output Set: N:\CRF3\12042001\I850991.raw

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200 GTC TTC AAT GTA TGT CCG TAC GAA GTG TCT ATA GAA ATC CCT GAT CTT     1536
201 Val Phe Asn Val Cys Pro Tyr Glu Val Ser Ile Glu Ile Pro Asp Leu
202             500             505             510
204 GCA TCA CTG CGG CTT CAG TTG CAT CCA GTG CAG GTG AAT TCA TCG GAT     1584
205 Ala Ser Leu Arg Leu Gln Leu His Pro Val Gln Val Asn Ser Ser Asp
206         515             520             525
208 GCG TTA GCC AGG CAG TCT GCG TAC GAC ACC GCC ACA GGT CGA TTC ACC     1632
209 Ala Leu Ala Arg Gln Ser Ala Tyr Asp Thr Ala Thr Gly Arg Phe Thr
210     530             535             540
212 GTG CCG AAA AGG ACA GCA GCA GTG TTC GTG GAA CCC AGG TGC T          1675
213 Val Pro Lys Arg Thr Ala Ala Val Phe Val Glu Pro Arg Cys
214 545             550             555
216 GATGGATGCC TTTCGCTAGC GAGCAAGTGC ATTCGGCATC CAAGTCGAAG CAAACGAATG     1735
218 AAATAAGAGA AGGCCATCGA ATAAAACGAA GTATATAAAT AGATTGAATA AGACGTTGCC     1795
220 CAAGTTGCCA AGGCACGCTT TGCCATATGT ATGCGTTGAA AAATAAATAA ATAAATAAAT     1855
222 AAATGATGTT ATAGAGGTAC AAAAGCATTG GAACATTTCT TTATAGAGGT GAACCACCCT     1915
224 ATTTTCCAGT TTCCATGTGT GAATTGTGAT TAGCATATGT ATGGAATAAT AATATAAATT     1975
226 AATTTTATGC AAAAAAAA                                                 1993
229 (2) INFORMATION FOR SEQ ID NO: 2:
231     (i) SEQUENCE CHARACTERISTICS:
232         (A) LENGTH: 558 amino acids
233         (B) TYPE: amino acid
234         (D) TOPOLOGY: linear
236     (ii) MOLECULE TYPE: protein
238     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
240 Gly Thr Arg Ser Lys Leu Pro Pro Gly Ser Asp Leu Gln Gln Ala Ala
241  1               5                   10                  15
243 Ile Val Ala Ile Gln Glu Glu Asp Pro Tyr Asn Trp Gly Tyr Asn Pro
244             20                  25                  30
246 Val Val Trp Gly Val Pro Lys Gly Ser Tyr Ala Ser Asn Pro Asp Gly
247         35                  40                  45
249 Pro Ser Arg Ile Ile Glu Tyr Arg Leu Met Val Gln Ala Leu Asn Arg
250     50                  55                  60
252 Leu Gly Leu Arg Val Val Met Asp Val Val Tyr Asn His Leu Tyr Ser
253 65                  70                  75                  80
255 Ser Gly Pro Phe Ala Ile Thr Ser Val Leu Asp Lys Ile Val Pro Gly
256             85                  90                  95
258 Tyr Tyr Leu Arg Arg Asp Ser Asn Gly Gln Thr Glu Asn Ser Ala Ala
259             100                 105                 110
261 Val Asn Asn Thr Ala Ser Glu His Phe Met Val Asp Arg Leu Ile Val
262         115                 120                 125
264 Asp Asp Leu Leu Asn Trp Ala Val Asn Tyr Lys Val Asp Gly Phe Arg
265     130                 135                 140
267 Phe Asp Leu Met Gly His Ile Met Lys Lys Thr Met Ile Arg Ala Lys
268 145                 150                 155                 160
270 Ser Ala Leu Gln Ser Leu Thr Ile Asp Glu His Gly Val Asp Gly Ser
271             165                 170                 175
273 Lys Ile Tyr Leu Tyr Gly Glu Gly Trp Asn Phe Gly Glu Val Ala Glu
274             180                 185                 190
```

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```
276 Asn Gln Arg Gly Ile Asn Gly Ser Gln Leu Asn Met Ser Gly Thr Gly
277         195             200             205
279 Ile Gly Ser Phe Asn Asp Arg Ile Arg Asp Ala Ile Asn Gly Gly Ser
280         210             215             220
282 Pro Phe Gly Asn Pro Leu Gln Gln Gly Phe Ser Thr Gly Leu Phe Leu
283 225             230             235             240
285 Glu Pro Asn Gly Phe Tyr Gln Gly Asn Glu Thr Glu Thr Arg Leu Thr
286         245             250             255
288 Leu Ala Thr Tyr Ala Asp His Ile Gln Ile Gly Leu Ala Gly Asn Leu
289         260             265             270
291 Lys Asp Tyr Val Val Ile Ser His Thr Gly Glu Ala Arg Lys Gly Ser
292         275             280             285
294 Glu Ile Arg Thr Phe Asp Gly Ser Pro Val Gly Tyr Ala Ser Ser Pro
295         290             295             300
297 Ile Glu Thr Ile Asn Tyr Ala Ser Ala His Asp Asn Glu Thr Leu Phe
298 305             310             315             320
300 Asp Ile Ile Ser Leu Lys Thr Pro Met Asp Leu Ser Ile Asp Glu Arg
301         325             330             335
303 Cys Arg Ile Asn His Leu Ser Thr Ser Met Ile Ala Leu Ser Gln Gly
304         340             345             350
306 Ile Pro Phe Phe His Ala Gly Asp Glu Ile Leu Arg Ser Lys Ser Leu
307         355             360             365
309 Asp Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Lys Ile Asp Phe
310         370             375             380
312 Thr Tyr Glu Thr Asn Asn Trp Gly Val Gly Leu Pro Pro Arg Glu Lys
313 385             390             395             400
315 Asn Glu Gly Ser Trp Pro Leu Met Lys Pro Arg Leu Glu Asn Pro Ser
316         405             410             415
318 Phe Lys Pro Ala Lys His Asp Ile Ile Ala Ala Leu Asp Lys Phe Ile
319         420             425             430
321 Asp Ile Leu Lys Ile Arg Tyr Ser Ser Pro Leu Phe Arg Leu Thr Thr
322         435             440             445
324 Ala Ser Asp Ile Val Gln Arg Val His Phe His Asn Thr Gly Pro Ser
325         450             455             460
327 Leu Val Pro Gly Val Ile Val Met Ser Ile Glu Asp Ala Arg Asn Asp
328 465             470             475             480
330 Arg His Asp Met Ala Gln Ile Asp Glu Thr Phe Ser Cys Val Val Thr
331         485             490             495
333 Val Phe Asn Val Cys Pro Tyr Glu Val Ser Ile Glu Ile Pro Asp Leu
334         500             505             510
336 Ala Ser Leu Arg Leu Gln Leu His Pro Val Gln Val Asn Ser Ser Asp
337         515             520             525
339 Ala Leu Ala Arg Gln Ser Ala Tyr Asp Thr Ala Thr Gly Arg Phe Thr
340         530             535             540
342 Val Pro Lys Arg Thr Ala Ala Val Phe Val Glu Pro Arg Cys
343 545             550             555
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346 (2) INFORMATION FOR SEQ ID NO: 3:
348   (i) SEQUENCE CHARACTERISTICS:
349   (A) LENGTH: 492 base pairs

VERIFICATION SUMMARY   DATE: 12/04/2001
PATENT APPLICATION: US/09/850,991   TIME: 13:25:27

Input Set : N:\Crf3\RULE60\09850991.txt
Output Set: N:\CRF3\12042001\I850991.raw

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L:10 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:63 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:358 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:376 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:380 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:384 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:389 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:393 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:397 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:401 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:405 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:409 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:413 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:417 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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